

RAW SEQUENCE LISTING

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Application Serial Number:

10/S95793

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DATE: 03/16/2007

PATENT APPLICATION: US/10/595,793

TIME: 12:30:00

Input Set : N:\efs\03_16_07\10595793_efs\101218_Sequence_List.txt

Output Set: N:\CRF4\03162007\J595793.raw

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3 <110> APPLICANT: ASTRAZENECA AB
4     Bostwick, Robert
5     Corradi, John
6     Defay, Thomas
7     Furlong, Stephen
8     Hirata, Lee T.
9     Ravyn, Vipa
10    Robbins, Alan
12 <120> TITLE OF INVENTION: GNAL Splice Variant and Uses Thereof
14 <130> FILE REFERENCE: 101218-1P US
16 <140> CURRENT APPLICATION NUMBER: 10/595,793
17 <141> CURRENT FILING DATE: 2006-05-11
19 <150> PRIOR APPLICATION NUMBER: 60/519,190
20 <151> PRIOR FILING DATE: 2003-11-11
22 <150> PRIOR APPLICATION NUMBER: 60/607,010
23 <151> PRIOR FILING DATE: 2004-09-03
25 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/004749
26 <151> PRIOR FILING DATE: 2004-11-11
28 <160> NUMBER OF SEQ ID NOS: 45
30 <170> SOFTWARE: PatentIn version 3.3
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33 <211> LENGTH: 1377
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
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42 gtccggggcg cgcgaaggga cacggcccgg accctgtctc ctcgggcgcg cgaaggagagc      180
44 ccggcatgcg ctcgcccaa agcagacaag ccgaaggaga agcggcagcg caccgagcag      240
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52 atcctgcacg tcaatgggtt taatcccagag gaaaagaaac agaaaattct ggacatccgg      480
54 aaaaatgtta aagatgctat cgtgacaatt gtttcagcaa tgagtactat aatacctcca      540
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64 ctctcagatg gcagattctt gacatctggg atttttgaga cacgattcca agtggacaaa      840
66 gtaaaacttc acatgtttga tgttggtggc cagagggatg agaggagaaa atggatccag      900
68 tgctttaacg atgtcacagc tatcatttac gtccgagcct gcagtagcta caacatggtg      960
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78 gccaaagtct ttatccggga cctgtttttg aggatcagca cggccaccgg tgacggcaaa 1260
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101 35 40 45
104 Ala Arg Thr Leu Leu Pro Arg Gly Gly Glu Gly Ser Pro Ala Cys Ala
105 50 55 60
108 Arg Pro Lys Ala Asp Lys Pro Lys Glu Lys Arg Gln Arg Thr Glu Gln
109 65 70 75 80
112 Leu Ser Ala Glu Glu Arg Glu Ala Ala Lys Glu Arg Glu Ala Val Lys
113 85 90 95
116 Glu Ala Arg Lys Val Ser Arg Gly Ile Asp Arg Met Leu Arg Asp Gln
117 100 105 110
120 Lys Arg Asp Leu Gln Gln Thr His Arg Leu Leu Leu Leu Gly Ala Gly
121 115 120 125
124 Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met Arg Ile Leu His Val
125 130 135 140
128 Asn Gly Phe Asn Pro Glu Glu Lys Lys Gln Lys Ile Leu Asp Ile Arg
129 145 150 155 160
132 Lys Asn Val Lys Asp Ala Ile Val Thr Ile Val Ser Ala Met Ser Thr
133 165 170 175
136 Ile Ile Pro Pro Val Pro Leu Ala Asn Pro Glu Asn Gln Phe Arg Ser
137 180 185 190
140 Asp Tyr Ile Lys Ser Ile Ala Pro Ile Thr Asp Phe Glu Tyr Ser Gln
141 195 200 205
144 Glu Phe Phe Asp His Val Lys Lys Leu Trp Asp Asp Glu Gly Val Lys
145 210 215 220
148 Ala Cys Phe Glu Arg Ser Asn Glu Tyr Gln Leu Ile Asp Cys Ala Gln
149 225 230 235 240
152 Tyr Phe Leu Glu Arg Ile Asp Ser Val Ser Leu Val Asp Tyr Thr Pro
153 245 250 255
156 Thr Asp Gln Asp Leu Leu Arg Cys Arg Val Leu Thr Ser Gly Ile Phe
157 260 265 270
160 Glu Thr Arg Phe Gln Val Asp Lys Val Asn Phe His Met Phe Asp Val
161 275 280 285
164 Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp Ile Gln Cys Phe Asn Asp
165 290 295 300
168 Val Thr Ala Ile Ile Tyr Val Ala Ala Cys Ser Ser Tyr Asn Met Val

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169 305          310          315          320
172 Ile Arg Glu Asp Asn Asn Thr Asn Arg Leu Arg Glu Ser Leu Asp Leu
173          325          330          335
176 Phe Glu Ser Ile Trp Asn Asn Arg Trp Leu Arg Thr Ile Ser Ile Ile
177          340          345          350
180 Leu Phe Leu Asn Lys Gln Asp Met Leu Ala Glu Lys Val Leu Ala Gly
181          355          360          365
184 Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu Tyr Ala Asn Tyr Thr Val
185          370          375          380
188 Pro Glu Asp Ala Thr Pro Asp Ala Gly Glu Asp Pro Lys Val Thr Arg
189 385          390          395          400
192 Ala Lys Phe Phe Ile Arg Asp Leu Phe Leu Arg Ile Ser Thr Ala Thr
193          405          410          415
196 Gly Asp Gly Lys His Tyr Cys Tyr Pro His Phe Thr Cys Ala Val Asp
197          420          425          430
200 Thr Glu Asn Ile Arg Arg Val Phe Asn Asp Cys Arg Asp Ile Ile Gln
201          435          440          445
204 Arg Met His Leu Lys Gln Tyr Glu Leu Leu
205          450          455
208 <210> SEQ ID NO: 3
209 <211> LENGTH: 1146
210 <212> TYPE: DNA
211 <213> ORGANISM: Homo sapiens
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216 cgacgcgagg ccaacaaaaa gatcgagaag cagttgcaga aagagcgcct ggcttacaag      120
218 gctaccaccc gctactgct cctgggggct ggtgagctct ggaaaagcac tatcgtcaaa      180
220 cagatgagga tcctgcacgt caatggggtt aatcccagag aaaagaaaca gaaaattctg      240
222 gacatccgga aaaatgttaa agatgctatc gtgacaattg tttcagcaat gactactata      300
224 atacctccag ttccgctggc caaccctgaa aaccaatttc gatcagacta catcaagagc      360
226 atagccccta tctactgact tgaatattcc caggaattct ttgaccatgt gaaaaaactt      420
228 tgggacgatg aaggcgtgaa ggcattgctt gagagatcca acgaatacca gctgattgac      480
230 tgtgcacaa acttcctgga aagaatcgac agcgtcagct tggttgacta cacaccacac      540
232 gaccaggacc tcctcagatg cagagttctg acatctggga tttttgagac acgattccaa      600
234 gtggacaaaag taaacttcca catgtttgat gttggtggcc agagggatga gaggagaaaa      660
236 tggatccagt gctttaacga tgtcacagct atcatttacg tcgcagcctg cagtagctac      720
238 aacatggtga ttcgagaaga taacaacacc aacaggctga gagagtcctt ggatcttttt      780
240 gaaagcatct ggaacaacag gtgggttacg accatttcta tcatcttggt cttgaacaaa      840
242 caagatatgc tggcagaaaa agtcttggca gggaaatcaa aaattgaaga ctatttccca      900
244 gaatatgcaa attatactgt tcctgaagac gcaacaccag atgcaggaga agatcccaaa      960
246 gttacaagag ccaagttctt tatccgggac ctgtttttga ggatcagcac ggccaccggt      1020
248 gacggcaaac attactgcta cccgcacttc acctgcgccg tggacacaga gaacatccgc      1080
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256 <211> LENGTH: 381
257 <212> TYPE: PRT
258 <213> ORGANISM: Homo sapiens
260 <400> SEQUENCE: 4

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263 1 5 10 15
266 Asp Glu Lys Glu Arg Arg Glu Ala Asn Lys Lys Ile Glu Lys Gln Leu
267 20 25 30
270 Gln Lys Glu Arg Leu Ala Tyr Lys Ala Thr His Arg Leu Leu Leu Leu
271 35 40 45
274 Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val Lys Gln Met Arg Ile
275 50 55 60
278 Leu His Val Asn Gly Phe Asn Pro Glu Glu Lys Lys Gln Lys Ile Leu
279 65 70 75 80
282 Asp Ile Arg Lys Asn Val Lys Asp Ala Ile Val Thr Ile Val Ser Ala
283 85 90 95
286 Met Ser Thr Ile Ile Pro Pro Val Pro Leu Ala Asn Pro Glu Asn Gln
287 100 105 110
290 Phe Arg Ser Asp Tyr Ile Lys Ser Ile Ala Pro Ile Thr Asp Phe Glu
291 115 120 125
294 Tyr Ser Gln Glu Phe Phe Asp His Val Lys Lys Leu Trp Asp Asp Glu
295 130 135 140
298 Gly Val Lys Ala Cys Phe Glu Arg Ser Asn Glu Tyr Gln Leu Ile Asp
299 145 150 155 160
302 Cys Ala Gln Tyr Phe Leu Glu Arg Ile Asp Ser Val Ser Leu Val Asp
303 165 170 175
306 Tyr Thr Pro Thr Asp Gln Asp Leu Leu Arg Cys Arg Val Leu Thr Ser
307 180 185 190
310 Gly Ile Phe Glu Thr Arg Phe Gln Val Asp Lys Val Asn Phe His Met
311 195 200 205
314 Phe Asp Val Gly Gly Gln Arg Asp Glu Arg Arg Lys Trp Ile Gln Cys
315 210 215 220
318 Phe Asn Asp Val Thr Ala Ile Ile Tyr Val Ala Ala Cys Ser Ser Tyr
319 225 230 235 240
322 Asn Met Val Ile Arg Glu Asp Asn Asn Thr Asn Arg Leu Arg Glu Ser
323 245 250 255
326 Leu Asp Leu Phe Glu Ser Ile Trp Asn Asn Arg Trp Leu Arg Thr Ile
327 260 265 270
330 Ser Ile Ile Leu Phe Leu Asn Lys Gln Asp Met Leu Ala Glu Lys Val
331 275 280 285
334 Leu Ala Gly Lys Ser Lys Ile Glu Asp Tyr Phe Pro Glu Tyr Ala Asn
335 290 295 300
338 Tyr Thr Val Pro Glu Asp Ala Thr Pro Asp Ala Gly Glu Asp Pro Lys
339 305 310 315 320
342 Val Thr Arg Ala Lys Phe Phe Ile Arg Asp Leu Phe Leu Arg Ile Ser
343 325 330 335
346 Thr Ala Thr Gly Asp Gly Lys His Tyr Cys Tyr Pro His Phe Thr Cys
347 340 345 350
350 Ala Val Asp Thr Glu Asn Ile Arg Arg Val Phe Asn Asp Cys Arg Asp
351 355 360 365
354 Ile Ile Gln Arg Met His Leu Lys Gln Tyr Glu Leu Leu
355 370 375 380
358 <210> SEQ ID NO: 5

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360 <212> TYPE: DNA

361 <213> ORGANISM: Mus musculus

363 <400> SEQUENCE: 5

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368 gagtgcagcg ctgcctccgg cgtcggcggg agccccggtc tgaccgcgcg ggacttgccc      180
370 gcgccccgcg ccccgatggg cctatgctac agcctgcggc cgctgctctt cgggagccca      240
372 gaggacaccc cgtgtgcggc ctcggaaccc tgcgcagagg atgctcagcc cagcgccgcc      300
374 ccggcccttg cctcgatccc agccccggct cccgtaggga ccttgcctcg gcgtggcggc      360
376 ggccggatcg tcgcgaacgc gcggccgcca ggcgagctgc agagccgccc gcgacaggag      420
378 cagctacgag ccgaggagcg cgaggcggtt aaagaggcga ggaaagttag cgggggcatc      480
380 gaccgcagtc tgcgcgagca gaagcgggac ctgcagcaga cgcaccggct cctgtctgtg      540
382 ggggctggtg agtcgggaaa aagcactatc gtcaaacaga tgaggatcct gcacgtcaat      600
384 ggcttcaacc ccgaggaaaa gaagcagaaa attctggaca tcaggaaaaa tgtcaaagat      660
386 gcgatcgtga caatcgtttc agcaatgagt actatcatac ctccagttcc actggccaac      720
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436 tcatcattta atgagttaat tctaagtgca ctggaacttt ctctgtgaag gtgaaactca     2220
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441 <210> SEQ ID NO: 6

442 <211> LENGTH: 230

443 <212> TYPE: PRT

444 <213> ORGANISM: Mus musculus

446 <400> SEQUENCE: 6

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449 1

5

10

15

VERIFICATION SUMMARY

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